

Query Match 11.3%; Score 571.8; DB 10; Length 654;
Best Local Similarity 95.3%; Pred. No. 3.8e-63;
Matches 622; Conservative 0; Mismatches 27; Indels 4; Gaps 3;
QY 4048 ttcgcgaacttacacgtgagcagaccagatggctgtcattcagttactcctgagtggtc 4107
Db 1 TTCCGCAACTTACACGTGGACGACAGATGGCTGTATTCAGTACTCCTGGATGGGCTC 60
QY 4108 atggtgtttgcagtggtgcagtcctcaccatgtaactccagatgctctacttc 4167
Db 61 ATGGTGTGTTCATGGGTGGCGATCCTCTCAAGAGTTTGGATGGCTCCAAATGCTACTTTC 120
QY 4168 gccctgatctgttttcaatgagtcacgcatgcacaaagtcctcagtgatgtacacccagtgt 4227
Db 121 GCCCTGATCTGGTTCATGAGTACCGCATGCACAAGTCCCGGATGTACAGCCAGTGT 180
QY 4228 gtccgaatgagccactctctcaagagtttggatggctcacaatcaccctccaggaaattc 4287
Db 181 GTCCGAATGAGCCACCTCTCTCAAGAGTTTGGATGGCTCCAAATGCTACTTTC 240
QY 4288 ctgtgcataaagacgtctactcttcacgattattccagtgatgggtggaataatcaa 4347
Db 241 CTGTGCATGAAAGCACGTCTACTCTTCAGCATTTATCCAGTGGTGGCTGGAATAATCAA 300
QY 4348 aaattcttgatgaacttcgaatgaactacatcaagaaactcagatcgtatcattgcatgc 4407
Db 301 AAATCTCTTGATGAACTCGAATGAACTACATCAAGAACTCGATGATCATTTGATGC 360
QY 4408 aaagaaaaatccacatcctgctcaagagcgtcttaccagctcacaagcctcctggac 4467
Db 361 AAAAGAAAAATCCACATCTGCTCAAGACGCTTCTACAGCTCACCAGCTCCTGGAC 420
QY 4468 tccgtgagcctattggagagagctgcatcagttcaacttttaacctgtaatacagttca 4527
Db 421 TCCGTGCAGCCTATTCGGAGAGAGCTGCATCAGTTTACCTTTTACCTTGTAAATCAAGTCA 480
QY 4528 cacatgtgagcgtggacttccgaaatgatgagagatcatctctgtgcaagtggccc 4587
Db 481 CACATGTGAGCGTGGAATTTCCGAAATGATGGCAGAAATCATCTCTGTCNAAGTGCCCC 540
QY 4588 aagatcctctctggg-aaagtcagccatctattt-ccacacccagtgaaagcattggaa 4645
Db 541 AAGATCTCTTTTGGGAAAGTCAAGCCCTCTTTTCCACACCCAGTGAAACCTTTGGAA 600
QY 4646 a--ccctatttcccaccagctcatgccccctttcaagatgctctctgcctg 4696
Db 601 AACCCCTTTTCCCCACCCCTTTTATGCCCCCTTTGAAAAAGCTTTTCTG 653

RESULT 2
AA524966/c 568 bp mRNA EST 05-AUG-1997
LOCUS nh35c11.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:954356
DEFINITION similar to gb:M23263 ANDROGEN RECEPTOR (HUMAN); mRNA sequence.
ACCESSION AA524966
VERSION AA524966.1 GI:2265894
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 568)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.
Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Prepared by: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 362 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 383.
Location/Qualifiers
1. 568
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:954356"
/clone_lib="NCI_CGAP_Pr3"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"
/note="Vector: pAMP10; Site_1: NotI; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from 5,000-10
000 microdissected cells histologically-determined to be
fully malignant prostate cancer cells. Double-stranded
cDNA was ligated to EcoRI adaptors, 5 cycles of PCR
applied to the cDNA with an adaptor-specific primer, and
the resulting PCR product subcloned into pAMP10 by the
UDG-cloning method (Life Technologies). Average insert
size is 600 bp. NOTE: Not directionally cloned. This
library was constructed by David Krizman."
BASE COUNT 186 a 99 c 153 g 130 t
ORIGIN

Query Match 9.9%; Score 501.4; DB 10; Length 568;
Best Local Similarity 98.5%; Pred. No. 2.9e-54;
Matches 527; Conservative 0; Mismatches 6; Indels 2; Gaps 2;
QY 4529 acatgtgagcgtgagcttccgaaatgatggcagagatcatctgtgcaagtgc-ccc 4587
Db 550 ACATGGTGAGCGTGACTTTCCGAAATGATGCCAGAGATCATCTCTGTGCAAGTGGCCCC 491
QY 4588 aagatcctcttctggaaagtcaagcccatctatttcacacccagtgaaagcattggaaac 4647
Db 490 AAGATCTCTTCTGGAAAGTCAAGCCCATCTATTTCCACACCCAGTGAAGCA-TGGAAAC 432
QY 4648 cctatttcccacacccagctcatgcccccttcagatgcttctgctgttataactctg 4707
Db 431 CCTATTCTCCACCCAGCTCATGCCCTTTTCAGATGCTCTCTGCTGTATATAACTCTG 372
QY 4708 cactactcctctgcagtcgttgggaatttcctctattatgatacagctgtgcatgaac 4767
Db 371 CACTACTCCTCTGCAGTGCCTTGGGAAATTTCCCTATTGATGTACAGTCTGTTCATGAAC 312
QY 4768 atgttctgaaattctatttgcgtgggctttttttctctctctctctctctctctctctc 4827
Db 311 ATGTTCTCGAATTTCTATTGCTGGGCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC 252
QY 4828 ttccctccctatctaaacctcccatggcaccttcagacttgccttgccttgccttgccttgcct 4887
Db 251 TTCCCTCCCTATCTAAACCTCCCATGGCACCTTCAGACTTTTGGCTTCCCATTTGGTGCCT 192
QY 4888 atctgtgtttgaaatggtgtgtatgcctttaactgtatgatacctcctcctatgctgcccag 4947
Db 191 ATCTGTGTTTGAATGTTGTGTATGCTTTTAAATCTGTGATGATCTCATATGAGGCCAG 132
QY 4948 tgcgaagtgtgctgttttacagcactactctgtgcagccacacacacacacacacacacacac 5007
Db 131 TGTCAAGTTGTGCTTGTATTACAGCAGTACTCTGTGGCAGCCACACAAACGCTTTTACTATC 72
QY 5008 ttatgcacacgggaagttaagagagcctaagattatctctgggaatacaacacacacacacacac 5062
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/clone_lib="NCI_CGAP_Pr3"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"
/notes="Vector: pAMP10; Site_1: Not1; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from 5,000-10
,000 microdissected cells histologically-determined to be
fully malignant prostate cancer cells. Double-stranded
cDNA was ligated to EcoRI adaptors, 5 cycles of PCR
applied to the cDNA with an adaptor-specific primer, and
the resulting PCR product subcloned into pAMP10 by the
UDG-cloning method (Life Technologies). Average insert
size is 600 bp. NOTE: Not directionally cloned. This
library was constructed by David Krizman."
BASE COUNT 77 a 113 c 72 g 126 t
ORIGIN

Query Match 7.5%; Score 380.6; DB 10; Length 388;
Best Local Similarity 99.0%; Pred. No. 5.6e-39;
Matches 383; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4442 tctaccagctcaccagctctggaacctcgtgagcctattgagagagctgcatcagt 4501
Db 2 TCGACCAAGCTCACCAGCTCTGGACTCCGCTCGGCTATTGGCAGAGAGCTGCATCAGT 61
Qy 4502 tcacttttgacctgcttaataaagtcacacatggtgagctggactttccgagaatagtg 4561
Db 62 TCCTTTTGACCTGCTAATCAAGTCACATGTGAGCGTGGACTTTCCGGAAATGATGG 121
Qy 4562 cagagatcatctgtgcaagtgcccaagatcctttctgggaaagtcaagcccatctatt 4621
Db 122 CAGAGATCATCTGTGCAAGTGCCCAAGATCCTTCTGGGAAAGTCAAGCCCATCTATT 181
Qy 4622 tccacacccagtggaagcttggaacctatttccccaccccaagctcagccctttca 4681
Db 182 TCCACACCCAGTGAAGCATTTGGAACCCCTATTTCGCCACCCGCTCATGCCCTTTCA 241
Qy 4682 gatgtctctgcctgttataactctgcaactcctctcgtcagtgcccttgggaattctct 4741
Db 242 GATGCTCTTCGCTGTATTAACCTGCACCTACTCTCTGCAGTGCCTTGGGGAATTCCT 301
Qy 4742 ctattgagtaagctctgcatgaacatgctcctgaattctatttctgggcttttttt 4801
Db 302 CTATTGATGATACAGTCTGTGATGAACATGTTCTGTAATTTCTATTGCTGGGCTTTT 361
Qy 4802 tctcttctctctctctctctctctctctctctctctctctctctctctctctctct 4828
Db 362 TCCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 388

RESULT 5
AA229062/c 369 bp mRNA EST 21-AUG-1997
LOCUS nc49q07.r1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1011516
DEFINITION similar to gb:M23263 ANDROGEN RECEPTOR (HUMAN);, mRNA sequence.
ACCESSION AA229062
VERSION AA229062.1 GI:1852046
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 369)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuvaqui, M.D.
, Michael Emmert-Buck, M.D., Ph.D.

```

cDNA Library Preparation: David B. Krizman, Ph.D.
 cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: -28ml3 revl ET from Amersham
 High quality sequence stop: 341.
 Location/Qualifiers
 1..369
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1011516"
 /clone_lib="NCI_CGAP_Pr3"
 /sex="Male"
 /dev_stage="45 years old"
 /lab_host="DH10B"
 /note="Vector: pAMP10; Site_1: Not1; Site_2: EcoRI; 1st
 strand cDNA was primed with oligo(dT)17 on 50 ng of
 DNase-treated, total cellular RNA obtained from 5,000-10
 ,000 microdissected cells histologically-determined to be
 fully malignant prostate cancer cells. Double-stranded
 cDNA was ligated to EcoRI adaptors, 5 cycles of PCR
 applied to the cDNA with an adaptor-specific primer, and
 the resulting PCR product subcloned into pAMP10 by the
 UDG-cloning method (Life Technologies). Average insert
 size is 600 bp. NOTE: Not directionally cloned. This
 library was constructed by David Krizman."

BASE COUNT 142 a 67 c 93 g 67 t
 ORIGIN

Query Match 7.3%; Score 369; DB 10; Length 369;
 Best Local Similarity 100.0%; Pred. No. 1.6e-37;
 Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4680 cagatgtcttctgctgttataaactctgcactactcctctcagtcgcttggggaatttc 4739
 Db 369 CAGAGTGTCTTCTGCTGTATTAACCTGCACCTACTCTCTGCAGTGCCTTGGGGAATTC 310
 Qy 4740 ctctattgagtaagctctgcatgaacatgttctcctgaattctatttctgggcttttt 4799
 Db 309 CTCTATTGATGATACAGTCTGTGATGAACATGTTCTCTGAATTTCTATTGCTGGGCTTTT 250
 Qy 4800 ttctcttct 4859
 Db 249 TTTCTCTTCT 190
 Qy 4860 tcagacttgccttcccatgttggtcctctctctctctctctctctctctctctctctctct 4919
 Db 189 TCAGACTTTGCTTCCCATTTGGCTCTCTATCTGTGTTTGAATGGTGTGTTATGCCCTTTA 130
 Qy 4920 aatctgtagatcctcatatgcccagtgctcaggtgtgcttctgttttacagcactactct 4979
 Db 129 AATCTGTGATGATCCTCATATGGCCAGTGTCAAGTTGTGCTTTGTATTACAGCACTACTCT 70
 Qy 4980 gtgcagccacacaaacgctttacttctatgccacgggaagtttagagagctaaagatt 5039
 Db 69 GTGCCACCCACACAAACGTTTACTTATCTTATGCCACGGGAAGTTTAGAGAGCTAAGATT 10
 Qy 5040 atctgggga 5048
 Db 9 ATCTGGGGA 1

RESULT 6
 T28396 413 bp mRNA EST 06-SEP-1995
 LOCUS EST41738 Human Uterus Homo sapiens cDNA 5' end similar to androgen
 DEFINITION receptor (HT:1334), mRNA sequence.
 ACCESSION T28396
 VERSION T28396.1 GI:610494
 KEYWORDS EST.

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SOURCE      human.
ORGANISM    Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 413)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult
,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W., Clayton,R.A.,
Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., FitzGerald
,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M., Glodek,A.,
Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinklejr,P.S., Kelley,J.M.,
Klinek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Otterback,T.R., Weidman,J.F., Li,F.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J.,
Dimke,D., Feng,P., Ferlie,A., Fischer,C., Hastings,G.A., He,W.-W.,
Hu,J.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A., Kozak,D.L.,
Kunsch,C., Ji,H., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei
,Y.-F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon
,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
Venter,J.C.
TITLE       Initial Assessment of Human Gene Diversity and Expression Patterns
JOURNAL     Based Upon 83 Million Basepairs of cDNA Sequence
MEDLINE     Nature 377, 3-174 (1995)
COMMENT     96026280
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@db.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@db.tigr.org)
Seq primer: M13 Reverse.

FEATURES             source
    source
    1..413
        /organism="Homo sapiens"
        /db_xref="ATCC (inhost):102309"
        /db_xref="taxon:9606"
        /clone_lib="Human Uterus"
        /note="Organ: uterus"
BASE COUNT    100 a 108 c 92 g 107 t 6 others
ORIGIN
Query Match      7.1%; Score 361; DB 11; Length 413;
Best Local Similarity 94.5%; Pred. No. 1.6e-36;
Matches 381; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

Qy 4047 ctccgcaattacaogtggacgaccagatggctgtcattcagctactcctgtatgggct 4106
Db 1 CTCCGCAACTTACACGTGGACGACCAGATGGCTGTNATTCAGTACTCCTGGATGGGCT 60
Qy 4107 catggttttgccatggctggcgatccttcaccaatgtcaactcagatgctctact 4166
Db 61 CATGGTGTGGCATGGCTGGCGATCCTTCACCAATGTNAACTCCAGGATGCTACTT 120
Qy 4167 cgccctgatctgttttcaatgagtaccgcatgcacaaagtcctccgcatgtacagccagt 4226
Db 121 CGCCCCNNACTGGTTTCAATGAGTACCGCATGCCACAACTCCCGGATGTACAGCCAGTC 180
Qy 4227 tgtccgaatgaggcacctctctcaagagtttggatggctcccaatcacccccaggaatt 4286
Db 181 TGTCGGAATGAGGCACCTCTCTCAAGAGTTTGGATGGCTCCAAATCACCCCCAGGAATT 240
Qy 4287 cctgtgatgaagcaactgtactcttcacgattattccagtgatggctgaaaaatca 4346
Db 241 CCTGTGATGAAGACACTGTCTACTTTCAGCATATTTCAGTGGGATGGGCTGAAAATCA 300
Qy 4347 aaaattcttgatgaacttcgaatgaactacatcaaggaactcgatcgatcatgttcgtg 4406
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Db 301 AAAATCTTTTGATGNACTTCGGATGNACTACA-CAAGGGACTCGGTGTAATTCATGTGATG 359
Qy 4407 caaaagaaaaaataccccatctctgctcaagacgctcttaccag 4449
|||||
Db 360 CAAAAGGAAAAATCCCATCTCTGNTTCAGACGGTTTTTACCAG 402

RESULT 7
AW619116 573 bp mRNA EST 24-MAR-2000
LOCUS 436 MARC PBE Sus scrofa cDNA 5', mRNA sequence.
DEFINITION AW619116
ACCESSION AW619116
VERSION AW619116.1 GI:7325300
KEYWORDS EST.
SOURCE Pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 573)
AUTHORS Smith,T.P.L., Fahrrenkrug,S.C., Rohrer,G.A., Simmen,F.A., Rexroad
,C.E. and Keele,J.W.
TITLE Mapping of expressed sequence tags from a porcine early embryonic
cDNA library
JOURNAL Anim. Genet. 32 (2), 66-72 (2001)
MEDLINE 21314990
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: GGAACAGCTATGACCATG
BACKWARD: GTAAACGACGGCCAGT
Seq primer: AATTAACCTCACTAAAGGG.

FEATURES             source
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        /tissue_type="Day 12 whole embryos"
        /lab_host="XL0LR"
        /note="Vector: pBLUESCRIPT SK-; Site_1: EcoRI; Site_2:
XhoI; Library made from pool of embryos in spherical and
filamentous stages of development (7.5% and 92.5%,
respectively, of each stage) as described in Choi et al,
Endocrinology 137, 1457-67, 1996."
BASE COUNT    125 a 199 c 162 g 87 t
ORIGIN
Query Match      7.1%; Score 358.4; DB 10; Length 573;
Best Local Similarity 77.7%; Pred. No. 3.1e-36;
Matches 471; Conservative 0; Mismatches 81; Indels 54; Gaps 1;

Qy 1863 gatggaatgcatgttaggctgggaagggtctacctcgcgcgcgcgcgcgcgcgcgcgcgc 1922
Db 10 GTTGAAGTGCAGTTAGGCTGGGAGGGTCTACCCCTTTCCGCTTCCAAAGACCTTTTCG 69
Qy 1923 aggaagctttccagaatctgttccagagcgtgcgaaagtatccagaacccggcccccag 1982
|||||
Db 70 AGGTGCTTTCAGAAACCTGTTCAAAGTGTAGCGGAAGTATCCAGAACCCAGGTTCCCGG 129
Qy 1983 gcaccagagccgcgagcagcacctccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 2042
|||||
Db 130 ACACCTTGAGGCCCGGCGGCGGAGCAGCCTCCCGGCCCGCTTTGACAGCAGCAGCTCA 189
Qy 2043 gcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2102
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Db 190 GCAGCAGGAGACCACTGCCCGCGCGCA----- 216

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KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
REFERENCE     1 (bases 1 to 349)
AUTHORS       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE         National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
JOURNAL       Unpublished (1997)
COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.
              , Michael Emmert-Buck, M.D., Ph.D.
              cDNA Library Preparation: David B. Krizman, Ph.D.
              DNA Sequencing by: Genome Systems Inc., Greg Lennon, Ph.D.
              Clone distribution: NCI-CGAP clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              www-bio.llnl.gov/bbrp/image/image.html
              Seq primer: -40m13 fwd. ET from Amersham
              High quality sequence stop: 230.

FEATURES      Location/Qualifiers
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               /clone="IMAGE:1011443"
               /clone_lib="NCI_CGAP_Pr3"
               /sex="Male"
               /dev_stage="45 years old"
               /lab_host="PH10B"
               /note="Vector: PAMP10; Site_1: NotI; Site_2: EcoRI; 1st
               strand cDNA was primed with oligo(dT)17 on 50 ng of
               DNase-treated, total cellular RNA obtained from 5,000-10
               ,000 microdissected cells histologically-determined to be
               fully malignant prostate cancer cells. Double-stranded
               cDNA was ligated to EcoRI adaptors. 5 cycles of PCR
               applied to the cDNA with an adaptor-specific primer, and
               the resulting PCR product subcloned into pAMP10 by the
               UDG-cloning method (Life Technologies). Average insert
               size is 600 bp. NOTE: Not directionally cloned. This
               library was constructed by David Krizman."
BASE COUNT    64 a 105 c 57 g 123 t
ORIGIN
Query Match      6.8%; Score 347.4; DB 10; Length 349;
Best Local Similarity 99.7%; Pred. No. 8.9e-35;
Matches 348; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4540 gtggaatttcggaaatgatggcagagatcatctctgtgcaagtgcccaagatcctttct 4599
Db 1 GTGGACTTTCGGAAATGATGGTAGAGATCATCTCTGTGCAAGTGCCCAAGATCCCTTTCT 60

Qy 4600 gggaaagtcaagccatctatttccacaccagtgagcattggaacccctatttcccca 4659
Db 61 GGGAAAGTCAAGCCATCTATTTCACACCCAGTGAAGCATTTGGAACCCCTATTTCCTCA 120

Qy 4660 cccagctatgcgccctttcagatgtcttctgcctgttataactctgcaactactctct 4719
Db 121 CCCAGCTCATGCCCTTTTCAGATGCTCTGCTGTATATACTCTGCACTACTCCTCT 180

Qy 4720 gcagtgccttggggaatttccctctattgatgtacagctctgtcatgaacatgttccctgaat 4779
Db 181 GCAGTGCCTTGGGGAATTTCTCTATTGATGTACAGTCTGTCAATGAACATGTTCCCTGAAT 240

Qy 4780 tctattgtcgggcttttttttttcttcttcttcttcttcttcttcttcttcttcttcttctt 4839
Db 241 TCTATTGCTGGGGCTTTTTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTAT 300

Qy 4840 ctaaccctcccatggcacccttcagaccttcttcccatgttgctccta 4888
Db 301 CTAACCCCTCCATGGCACCTTCAGACTTTGCTTCCCATTTGCTGCTCCTA 349

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RESULT 10
AA659567/c
LOCUS    AA659567      379 bp      mRNA      EST      05-NOV-1997
DEFINITION nt63a03.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1203148
              similar to gb:M23263 ANDROGEN RECEPTOR (HUMAN);, mRNA sequence.
ACCESSION AA659567
VERSION    AA659567.1 GI:2595721
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 379)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL      Unpublished (1997)
COMMENT      Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.
            , Michael Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: David B. Krizman, Ph.D.
            DNA Sequencing by: Genome Systems Inc., Greg Lennon, Ph.D.
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 360.

FEATURES      Location/Qualifiers
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               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone="IMAGE:1203148"
               /clone_lib="NCI_CGAP_Pr3"
               /sex="Male"
               /dev_stage="45 years old"
               /lab_host="DH10B"
               /note="Vector: PAMP10; Site_1: NotI; Site_2: EcoRI; 1st
               strand cDNA was primed with oligo(dT)17 on 50 ng of
               DNase-treated, total cellular RNA obtained from 5,000-10
               ,000 microdissected cells histologically-determined to be
               fully malignant prostate cancer cells. Double-stranded
               cDNA was ligated to EcoRI adaptors. 5 cycles of PCR
               applied to the cDNA with an adaptor-specific primer, and
               the resulting PCR product subcloned into pAMP10 by the
               UDG-cloning method (Life Technologies). Average insert
               size is 600 bp. NOTE: Not directionally cloned. This
               library was constructed by David Krizman."
BASE COUNT    130 a 67 c 95 g 87 t
ORIGIN
Query Match      6.8%; Score 346; DB 10; Length 379;
Best Local Similarity 98.1%; Pred. No. 1.3e-34;
Matches 371; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

Qy 4705 ctgcactactctctgcagtgcccttgggggaatttctctattgatgtacagtctgtcatg 4764
Db 376 CTGCACACTACTCTCTGCAGTGCCTTGGGGAATTTCTCTATTGGTGTACAGTCTGTCTATG 317

Qy 4765 aacatgttctgaattctatttctgtgggcttttttttctcttcttcttcttcttcttctt 4824
Db 316 AACATGTTCTCTGAATCTATTGTGGGC-TTTTATCTCTCTCTCTCTCTCTCTCTCTCTTTC 258

Qy 4825 ttcttctctccctatctaaacctcccatggcaccttcagaccttcttcttcttcttcttcttct 4884
Db 257 CTCCTTCCCTCCCTATCTAACCTCCCATGGCACCTTCAGACTTGTCTTCCCATGTGGCT 198

Qy 4885 cctatctgtgttttgaatgggtgttgatgcctttaaactgtgatcctcatatgccc 4944

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[illegible]

Clones are derived from the mouse BAC library RCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Plate: 259 row: K column: 23
 Seq primer: T7
 Class: BAC ends.

FEATURES	SOURCE
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-259K23"
/clone_lib="RPCI-23"
/sex="Female"
/lab_host="DH10B"
/note="organ: Kidney/brain; Vector: pBAC3.6; Site.1:
EcoRI; Site.2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBAC3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."
102 a 173 c 147 g 75 t 1 others

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Query Match 5.8%; Score 293.2; DB 13; Length 498;
Best Local Similarity 73.9%; Pred. No. 5.3e-28;

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1925	QY	qagctttccaaatctgttcagagctgcgcaagtgtaccagaaccgcggcccgagc	1984
61	Db	GAGCGTTCAGAACTGTGTCAGAGCTGGCGAAGCGATCCAGAACCCGGGCCCGAGC	120
1985	QY	accagagcgcgagcagcagcaactcccgcgcagctttgtgctgcgcagcagc	2044
121	Db	ACCTTGAGGCGCTAACATAGCACTCCGGGCGCTGTTT-----	160
2045	QY	agcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc	2104
161	Db	-----ACAGCAGAGC	171
2105	QY	agcaagagactagccccagcagcagcagcagcagcagctgagtggtctcccccag	2164
172	Db	AGAGTCNAGCCCCCGCGCGGTGGCGAGCAGCACTGAGGATGGTTCCTCTCAG	231
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232	Db	CCACATCAGAGGCCCCACAGGCTACCTGGCCCTGGAGGAGGAACAGCACTTCACAGC	291
2225	QY	cgagtcggccctgaagtgcacccccagagagagtgcgtccacagagctcgagccgcg	2284
292	Db	AGCAGGACGCTCCGAGGGCCACCTTGAGAGACGCTGCCCTCCCGAGGCTGGGGCGGCCA	351
2285	QY	tgqccgcagcaaggggtgcgcgagcagctgcgcagcactccgcgacgagatgactcag	2344
352	Db	CGCTCCTGGCAAGGGGTGGCGAGCCACCACGCTCCTCCAGATCAGGATGACTCAG	411
2345	QY	ctgcccatccacgttgtccctgtcgtggcccccactttcccgcgttaagcagctgcctcg	2404
412	Db	CTGCCCCATCCAGTTGTCCTGTGGGCCCCACTTTCACAGGCTTAAGCAGCTGCTCCG	471
2405	QY	ctgaccttaagacatcctgcgcgagg	2431
472	Db	CCGACATTTAAAGACATTTTGACAGG	498

RESULT 13
AA229714/C

LOCUS AA229714 292 bp mRNA 20-AUG-1997
DEFINITION NC1_CGAP_P3 Homo sapiens cDNA Clone IMAGE:1011443
similar to gb:M32363 (HUMAN);, mRNA sequence.
ACCESSION AA229714
VERSION AA229714.1 GI:1851877
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 292)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.
, Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 250.

FEATURES	SOURCE
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100. <i>Other</i>	

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   /dev_stage="45 years old"
   /lab_host="DH10B"
   /note="vector: pAMP10; Site_1: NotI; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from 5,000-10
,000 microdissected cells histologically-determined to be
fully malignant prostate cancer cells. Double-stranded
cDNA was ligated to EcoRI adaptors, 5 cycles of PCR
applied to the cDNA with an adaptor-specific primer, and
the resulting PCR product subcloned into pAMP10 by the
UDG-cloning method (Life Technologies). Average insert
size is 600 bp. NOTE: Not directionally cloned. This
library was constructed by David Krizman."

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BASE COUNT	107 a	50 c	73 g	62 t
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Query Match	5.6%	Score 285.4;	DB 10;	Length 292;
Best Local Similarity	99.7%	Pred. NO. 6.1e-27;		
Matches 286;	Conservative	0; Mismatches	1; Indels	0; Gaps

[illegible]

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Db 187 CCTATCTGTGTTTGAATGGTGTGTATGGCTTTAAATCTGTGATGATCCTCATATGGCC 128
QY 4945 cagtgtcaagttgtgcttgtttacagcaactactctgtgccagccacacaaacgtttactt 5004
Db 127 CAGTGTCAAGTTGTGCTTGTTTACAGCACTACTCTGTGCCAGCCACACAAACGTTTACTT 68
QY 5005 atcttatgccacgggaagtttagagagcctaagattatctt9999aaatcaaaacaaaaa 5062
Db 67 ATCTTATGCCACGGGAAGTTTAGAGAGCTAAGATTATCTGGGGAATCAAAACAAAAA 10

Search completed: January 3, 2002, 20:10:32
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